

# Using the new R package for TL dating

D. Strebler, D. Brill, C. Burow, H. Brückner

## 3. Data pretreatment

Unlike OSL data where luminescence signal and background (BG) information are extracted from the same decay curve, TL data require the combination of different records. Moreover, when the TL signal is recorded during the preheat, the preheat curves and the curves that will be used to estimate the  $D_e$  must be properly identified. Finally, heating rates can vary between successive TL readings and can influence peak position, hence, data pretreatment is needed.

The `script_TL.pretreatment` function calls `script_TL.input` and a series of functions that do this data treatment: (1) separate the preheat curves from the TL curves (Fig. 3); (2) subtract the BG signal from the TL signal and (3) align the peak maximum using the TL ( $L_x$ ) or the test dose ( $T_x$ ) signal as reference (Fig. 4). Once the data pretreatment is finished, the function creates a new `.binx` file with the modified luminescence curves.

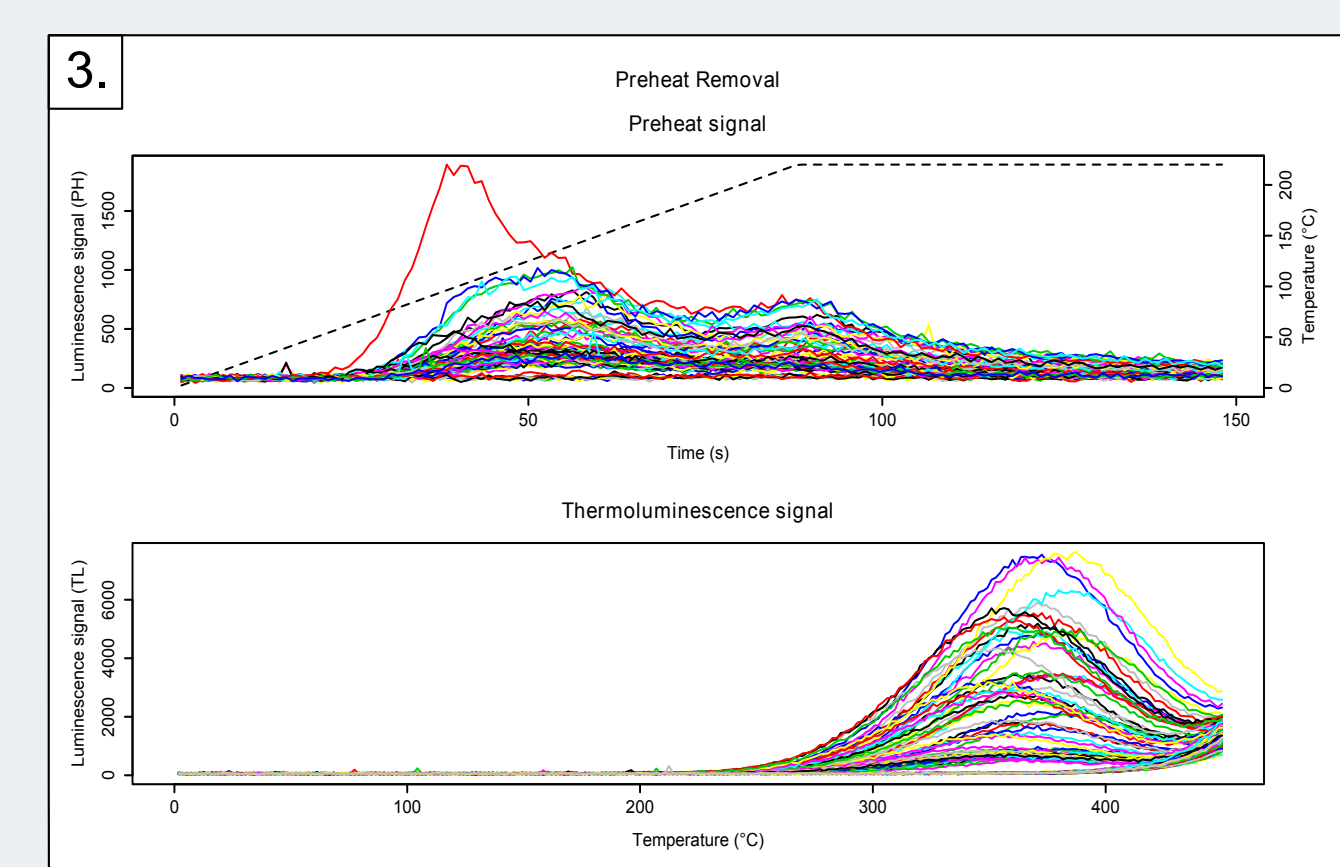


Fig 3. Plot of the preheat and the signal curves (mod\_remove.preheat).

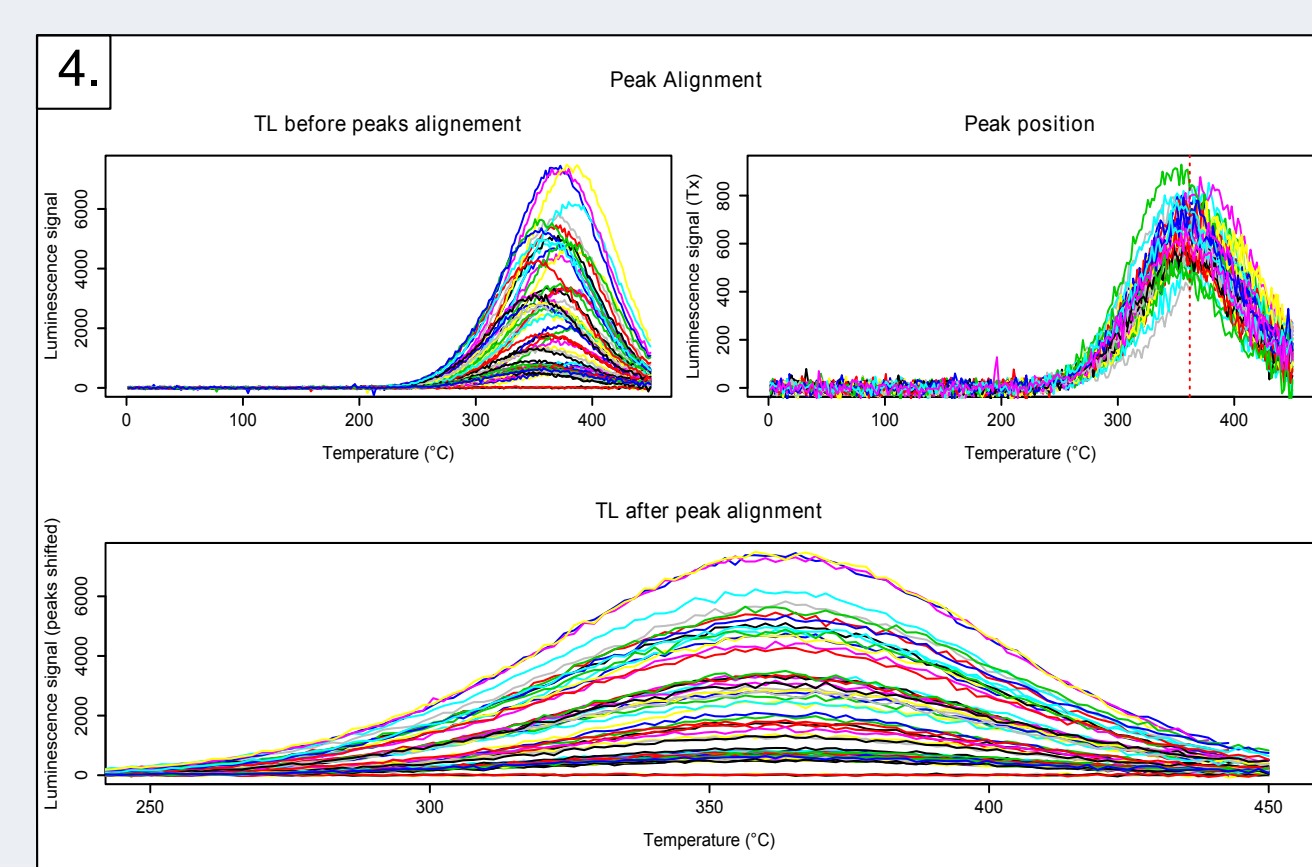


Fig 4. Plot of the TL curves after peak alignment (mod\_align.peak).

## 4. The heating plateau test

When working with heated material, like burnt flint or ceramics, it is required to make a heating plateau test, even if the dating is done using OSL. This test allows us to verify if the signal was properly reset during the initial heating.

The `script_TL.plateau` function first calls `script_TL.pretreatment` to open the specified file and makes the required data pretreatment. Then it calls `analyse_TL.plateau` which divides the average natural signal ( $L_n$ ) by each of the average additive dose signals ( $L_x$ ) available (Fig. 5). When the additive curves are followed by test dose curves ( $T_x$ ), the function also estimates the ratio between  $L_n/T_n$  and  $L_x/T_x$  (Fig. 6).

If  $L_n/L_x$  and  $(L_n/T_n)/(L_x/T_x)$  present a plateau when  $L_x$  presents a peak, it means that the sample was properly reset and TL or OSL dating should be possible [3].

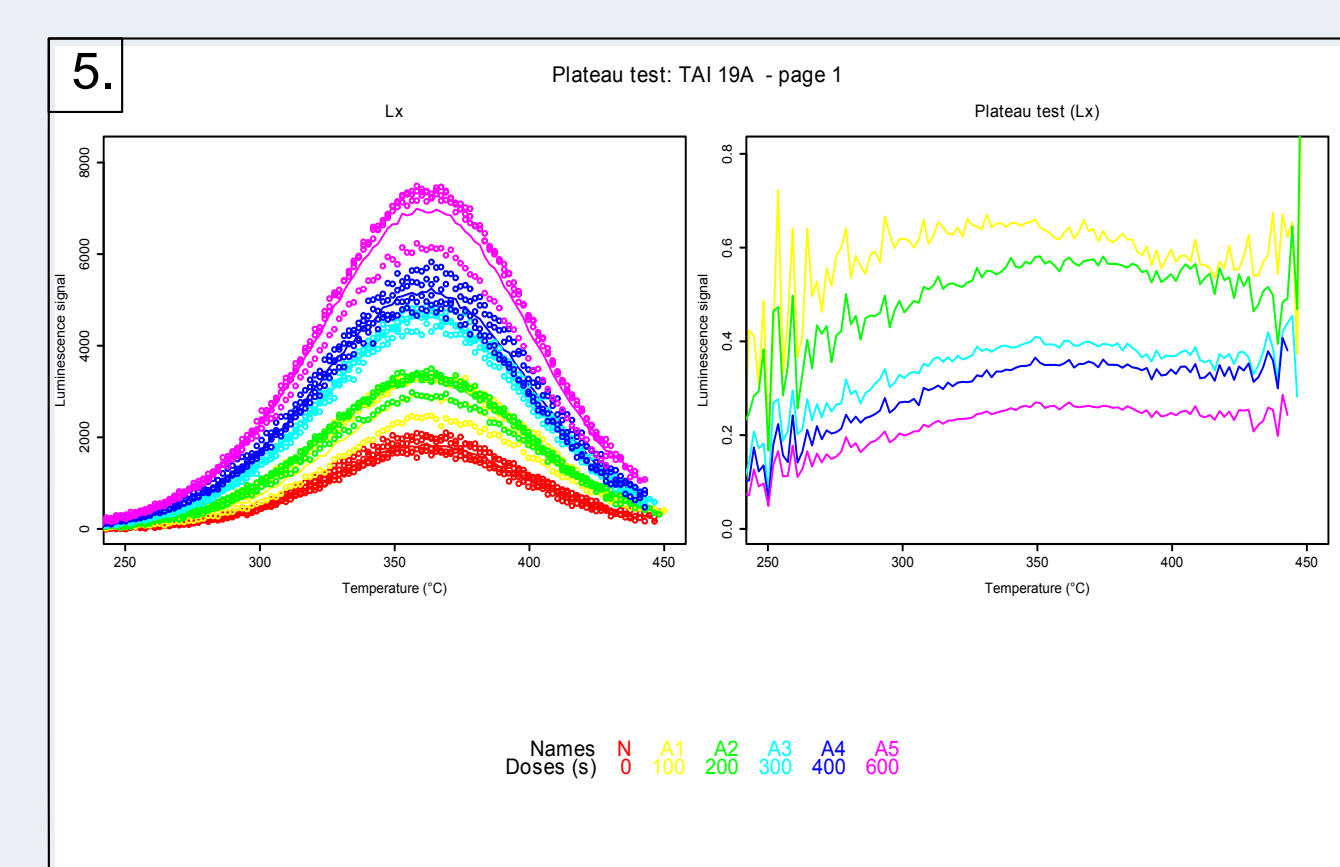


Fig 5.  $L_x$  and  $L_n/L_x$  vs. temperature. (a)  $L_x$  has a peak maximum around 360 °C; (b)  $L_n/L_x$  is nearly constant between 340°C and 400 °C.

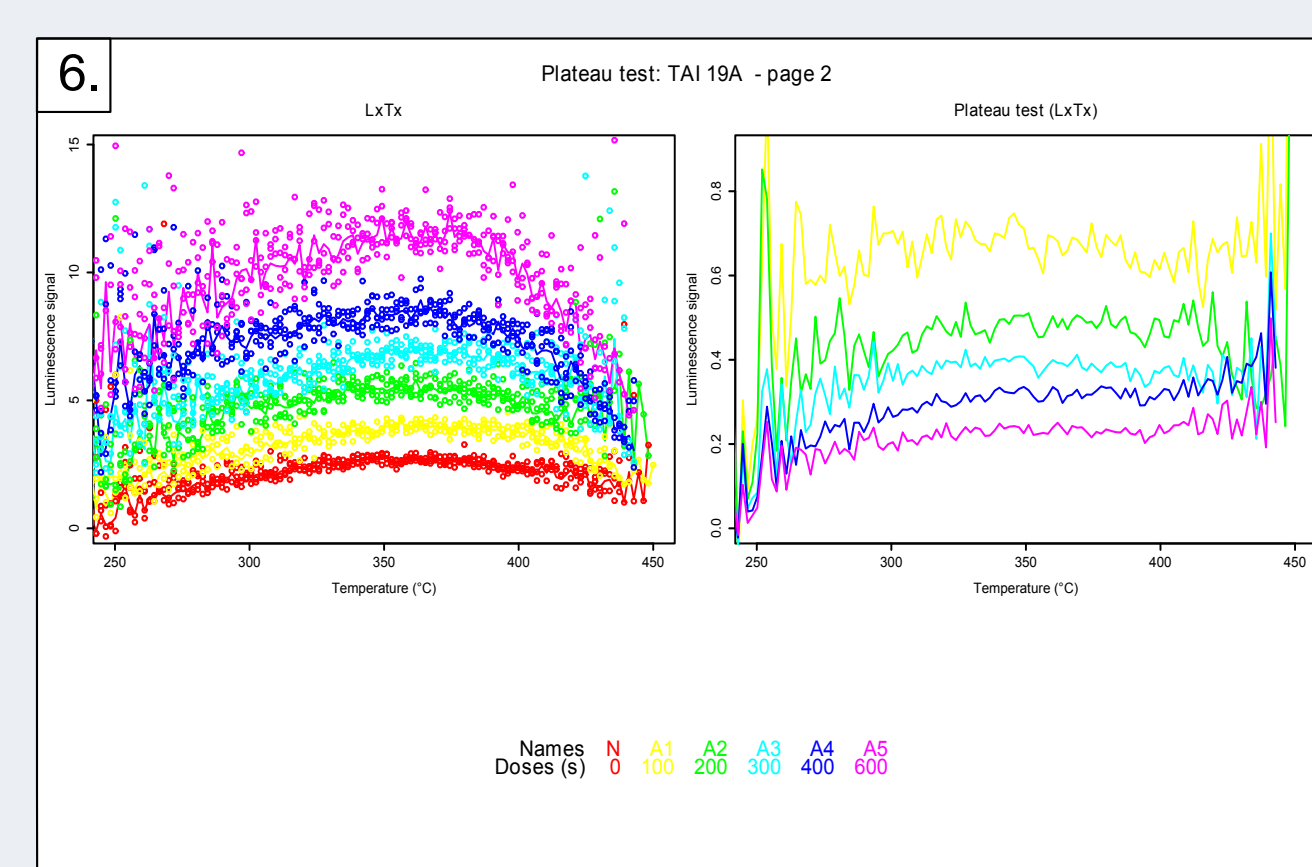


Fig 6.  $L_x/T_x$  and  $(L_n/T_n)/(L_x/T_x)$  vs. temperature. (a)  $L_x/T_x$  has a peak maximum around 360 °C; (b)  $(L_n/T_n)/(L_x/T_x)$  is constant between 340 °C and 400 °C.

## 1. Introduction

R is an extremely versatile programming language and environment for statistical computing and graphics. It allows users to make their own sets of functions and to share them with the community. A package for luminescence dating is already available [1], but it mainly includes tools for OSL dating with the single aliquot regenerative dose (SAR) protocol [2].

The aim of this project is to implement a new package specifically designed for thermoluminescence dating (TL). This package will include functions to perform TL curve pretreatment, the heating plateau test and  $D_e$  estimation with both the multiple aliquot additive dose (MAAD) [3] and the SAR protocols [4].

## 2. Starting with TLdating

One of the main ideas behind this project is to make a package that is as easy to use as possible. Five `script_*` functions are included. They aggregate the operations needed for different applications (Fig. 1):

- (1) `script_TL.input` allows import of a `.binx` file into R (Fig. 2);
- (2) `script_TL.pretreatment` creates a new `.binx` file after a series of predefined data manipulations;
- (3) `script_TL.plateau` realises a heating plateau test;
- (4) `script_TL.MAAD` and (5) `script_TL.SAR` estimate the palaeodose using the MAAD and the SAR protocol respectively.

To import TL curves, each function only needs the file name and the relative uncertainty of the data. The required parameters have been reduced as much as possible but complementary parameters allow the result to be refined.

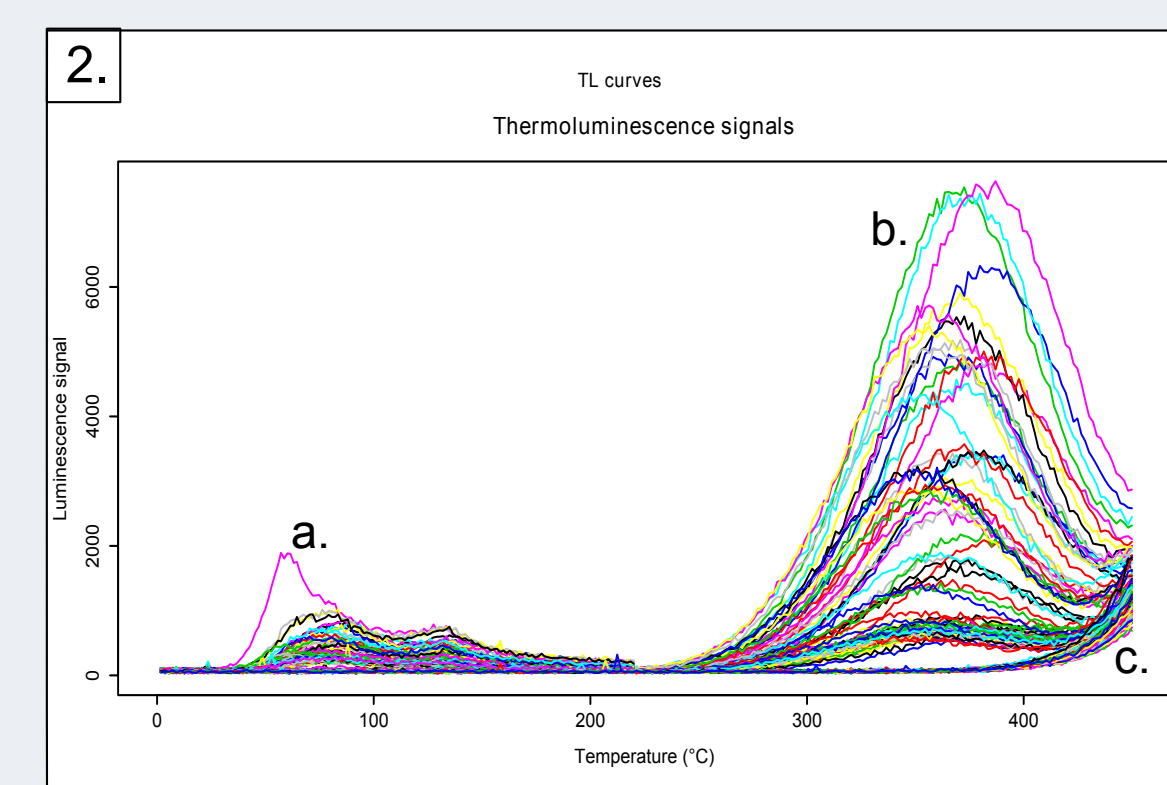
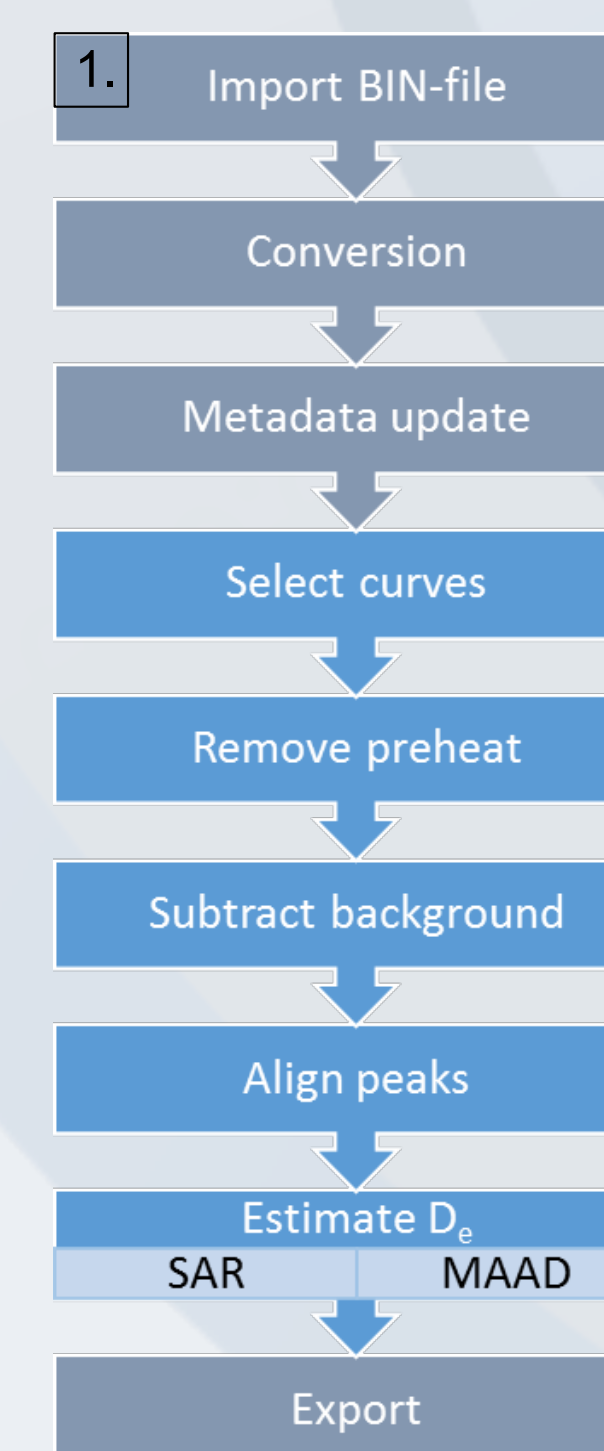


Fig 1. Workflow followed by the `script_*` functions. First, the BIN-file is imported and converted into the proper format, the metadata are updated and the undesirable curves removed. When only the relevant data remain, they are combined, first, to produce a better signal, then, to estimate the palaeodose. Finally, the results are exported.

Fig 2. Plotting of the TL curves after being imported by `script_TL.input`. It is possible to identify (a) preheat curves, (b) signal curves and (c) background curves.



## 7. Results and discussion

The `TLdating` package was used to estimate the equivalent dose ( $D_e$ ) of five heated silex artefacts coming from the Palaeolithic site of Taibeh, Jordan. These artefacts were associated with the Masraqan technocomplex, currently dated between 16 and 20 ka BC (MIS 2).

When using `Analyt` on the same dataset, similar  $D_e$  values were obtained. Our package produces slightly lower  $D_e$  values which could be linked to the methods used by the two programs to process the background signal.

The difference between SAR-TL and MAAD-TL is generally below  $\pm 5\%$ , both protocols provide reliable results. SAR-TL is more time consuming, but needs less material. The dose plateau approach clearly helps to select the best temperature interval. A divergence between the DP and the GC results for MAAD-TL generally means a divergence between SAR-TL and MAAD-TL.

## 5. The MAAD protocol

The MAAD protocol was developed at the beginning of luminescence dating but is still widely used for TL dating [3]. With this protocol, the  $D_e$  is the sum of a palaeodose ( $Q$ ), estimated using a series of natural aliquots irradiated by additive doses, and a sublinearity correction ( $I$ ), estimated using bleached aliquots irradiated by regenerative doses. Each additive and regenerative dose signal ( $L_x$ ) can be followed by a test dose signal ( $T_x$ ) to normalise the results.

The `script_TL.MAAD` function begins by calling `script_TL.pretreatment` to open the file and preprocess the data. Then it calls `analyse_TL.MAAD` which plots  $L_x$ ,  $T_x$ ,  $L_x/T_x$  and their respective heating plateau, for the additive curves (Fig. 7) and the regenerative curves, and estimates the  $D_e$  using the growth curve (GC) and the dose plateau (DP) approach (Fig. 8).

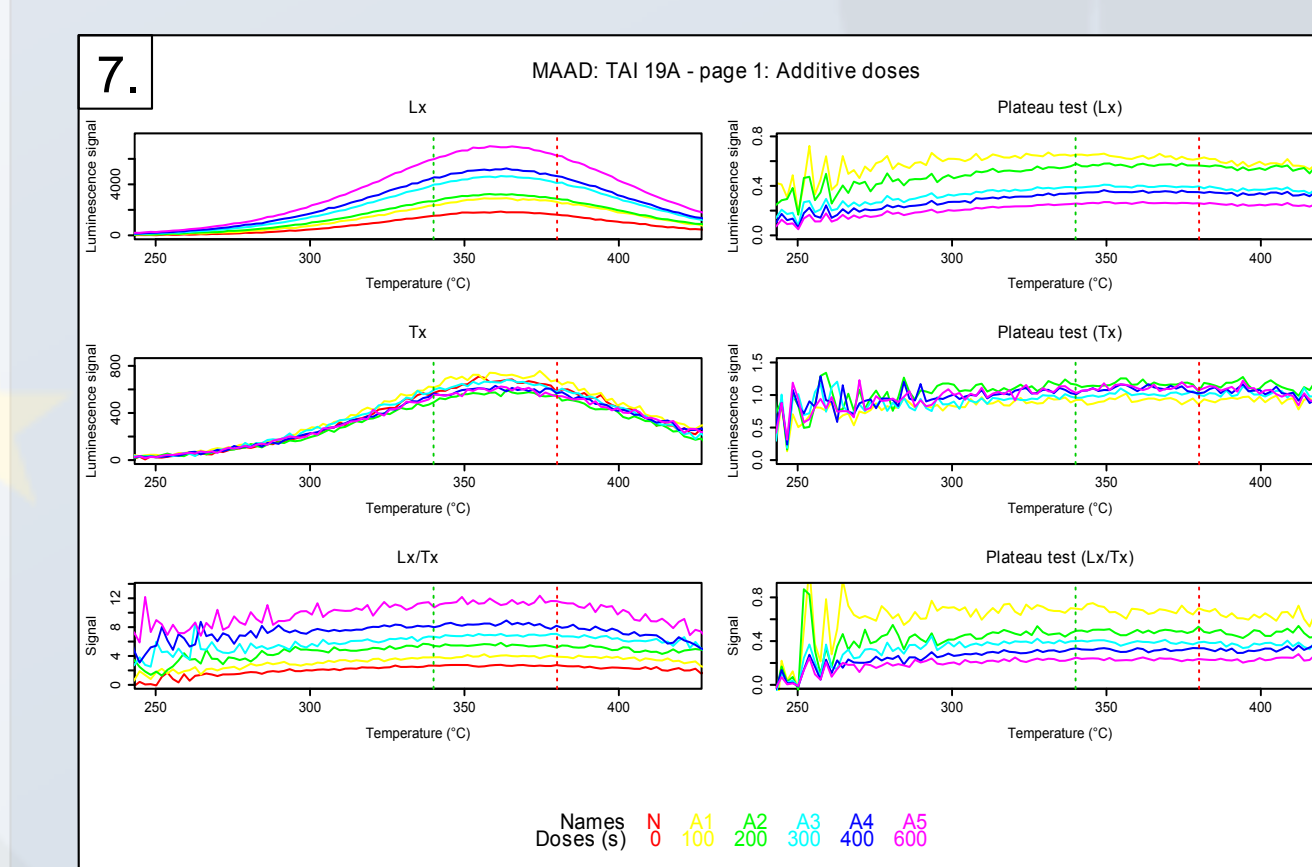


Fig 7.  $L_x$ ,  $T_x$ ,  $L_x/T_x$  and their respective heating plateau test for the additive dose steps of the MAAD protocol.

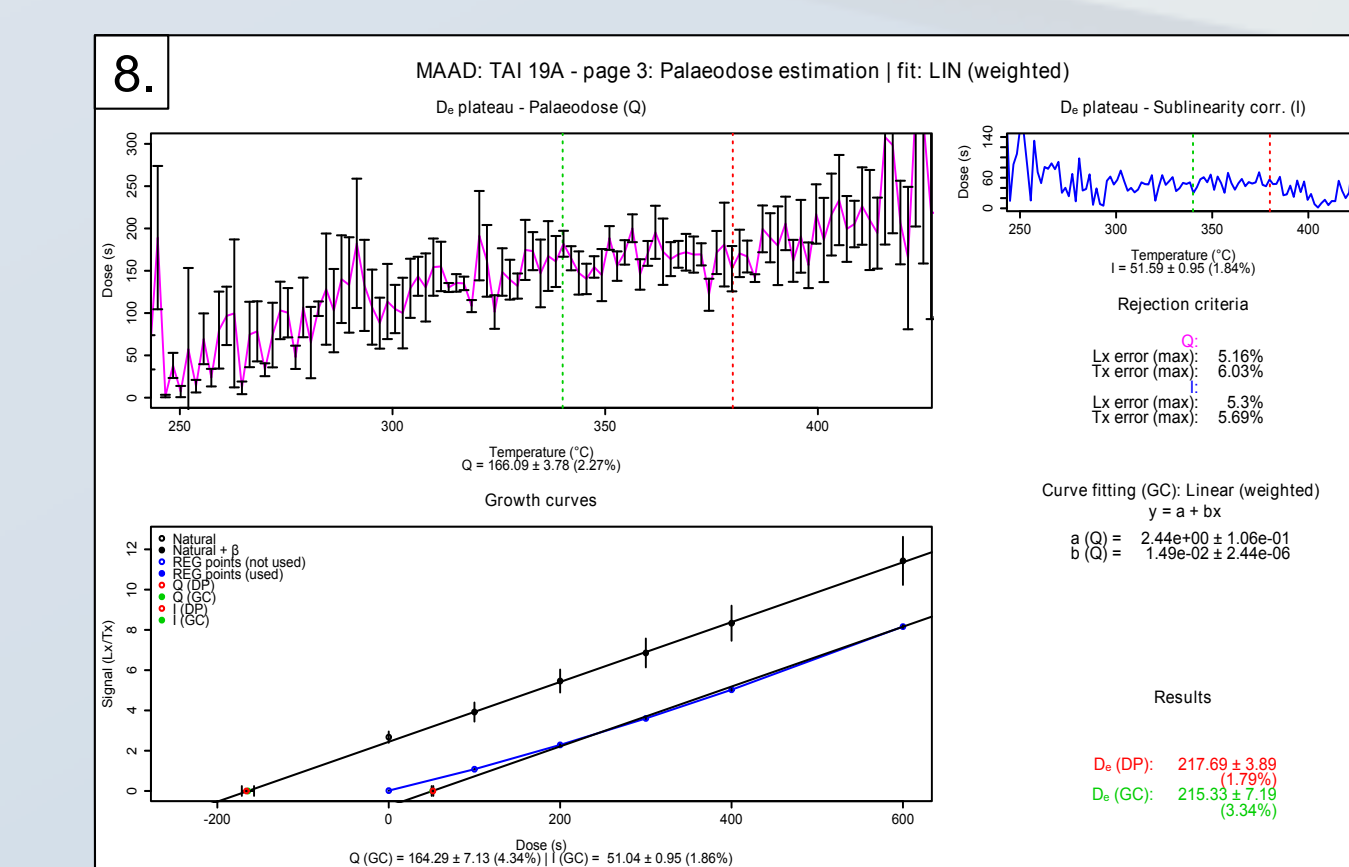


Fig 8. Estimation of the Palaeodose ( $Q$ ) and the sublinearity correction ( $I$ ) using the dose plateau (DP) and the growth curve (GC) approaches. The final  $D_e$  is the sum of  $Q$  and  $I$ .

## 6. The SAR protocol

The SAR protocol was initially designed for OSL dating. However, it can be easily adapted for TL dating. The  $D_e$  is estimated by comparing the natural signal to a growth curve generated by irradiating the same aliquot with a series of regenerative doses. Each regenerative dose is followed by a testdose to normalise the results and correct sensitivity changes.

Once again, the `script_TL.SAR` function first calls `script_TL.pretreatment` to open the file and preprocess the data. Then it calls `analyse_TL.SAR`. For each aliquot, this function plots  $L_x$ ,  $T_x$ ,  $L_x/T_x$  and their respective heating plateau curves, and estimates the  $D_e$  using a growth curve (GC) and a dose plateau (DP) approach (Fig. 9).

The  $D_e$  values of the different aliquots can be combined using a dedicated function from the `Luminescence` package, for example, `plot_AbanicoPlot` (Fig. 10).

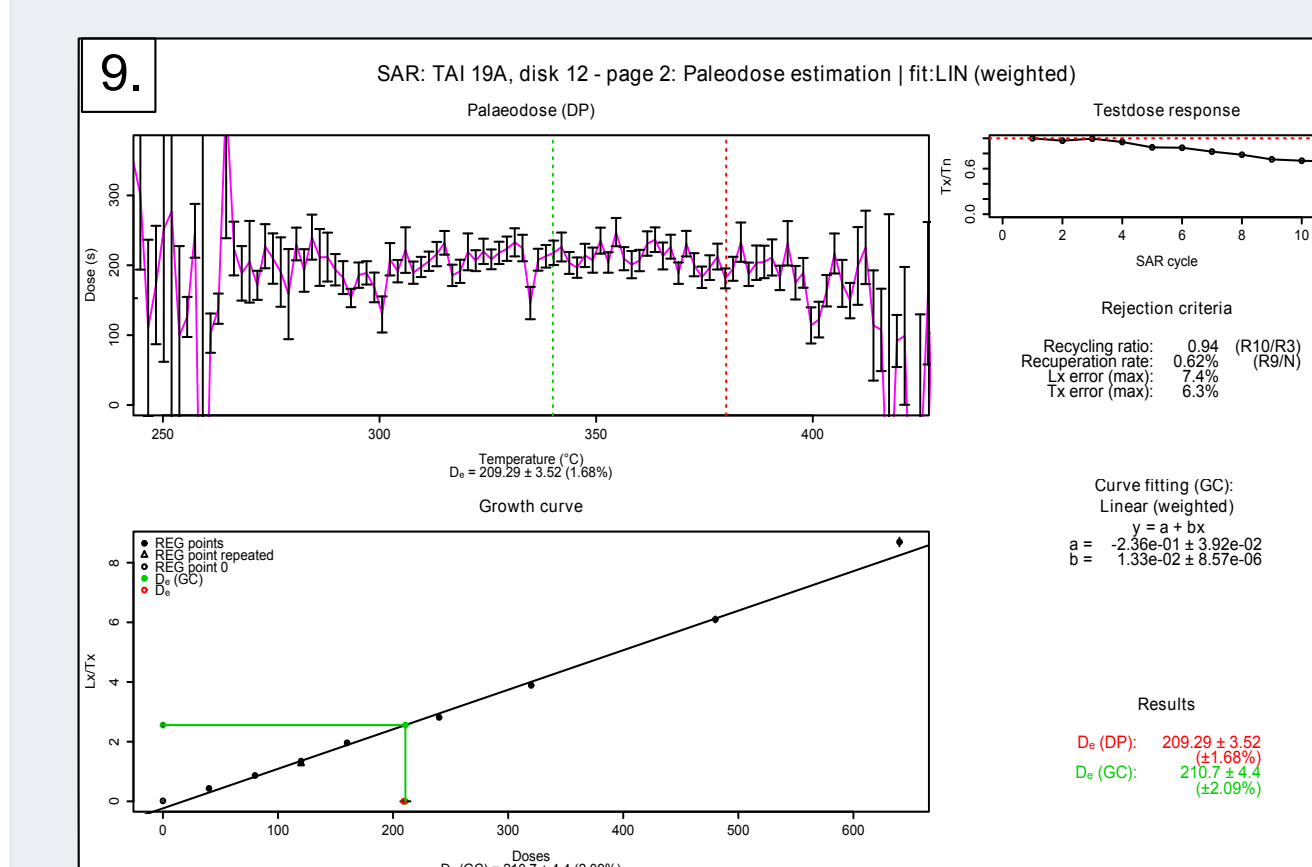


Fig 9. Estimation of the  $D_e$  using the dose plateau (DP) and the growth curve (GC) approaches. In the upper right corner, we can see the evolution of the testdose response ( $T_x/T_n$ ).

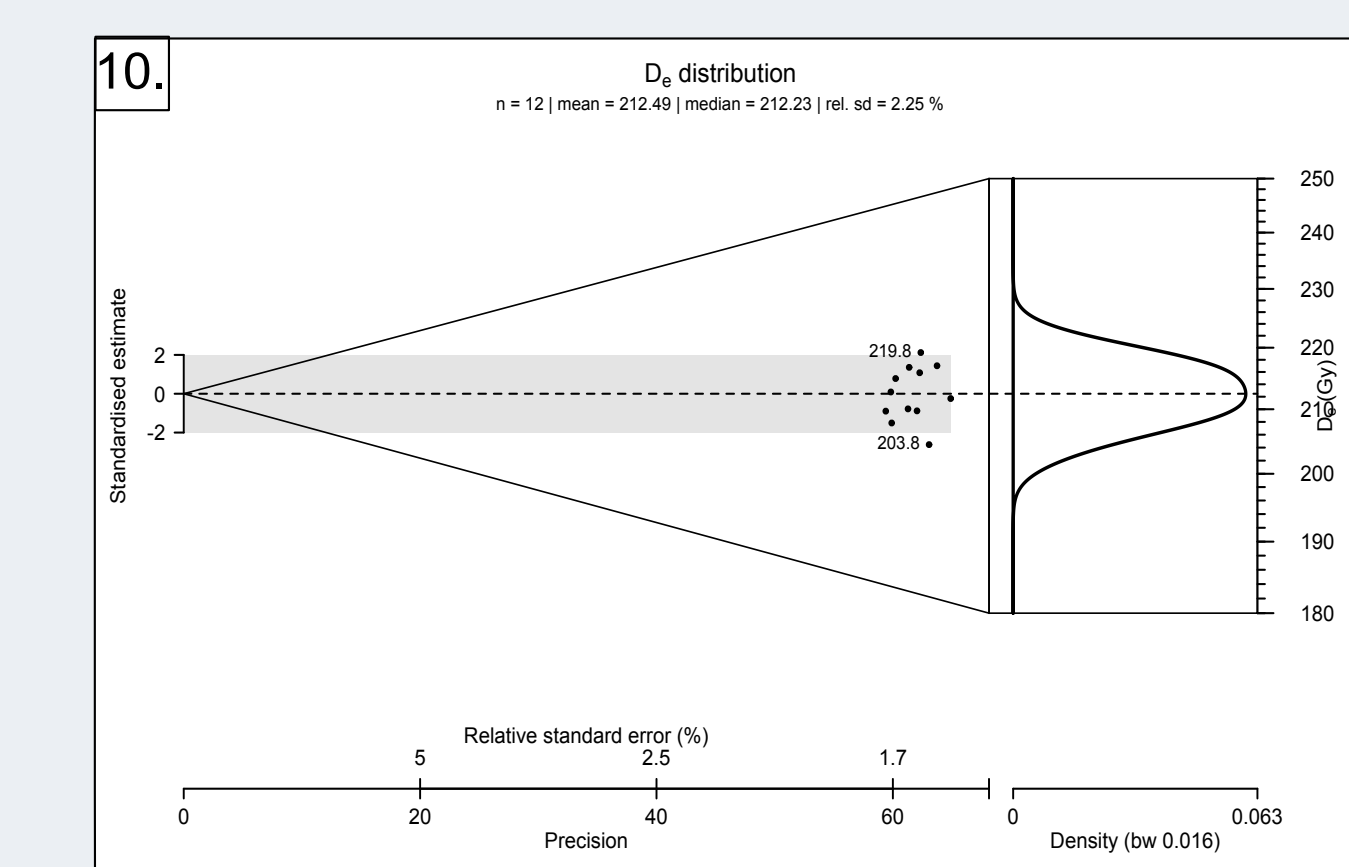


Fig 10. Example of  $D_e$  distribution using the abanico plot for 12 aliquots from the same sample using the dose plateau approach.

### Bibliography

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Institute of Geography, University of Cologne, Albertus-Magnus-Platz, D-50923 Köln -

[www.geographie-koeln.de](http://www.geographie-koeln.de)

Contact: David Strebler, [david.strebler@uni-koeln.de](mailto:david.strebler@uni-koeln.de).

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You can find more information about the CRC 806 on: <http://www.sfb806.uni-koeln.de>

